AMENDMENTS TO THE CLAIMS

1.   (Original) A process for preparing amino acids selected from the group of methionine, homoserine and lysine in transgenic organisms, wherein the process comprises the following steps:

   a)   introduction of a nucleic acid sequence which codes for a threonine-degrading protein or lysine-degrading protein or codes for a threonine-degrading protein and lysine-degrading protein, or

   b)   introduction of a nucleic acid sequence which increases threonine degradation or lysine degradation or threonine degradation and lysine degradation in the transgenic organisms, and

   c)   expression of a nucleic acid sequence mentioned under (a) or (b) in the transgenic organism.

2.   (Currently amended) A process for preparing amino acids in transgenic organisms as claimed in claim 1, wherein the process comprises the following steps, solved:

   a)   introduction of a nucleic acid sequence which codes for a threonine-degrading protein which comprises the following consensus sequence

   $H[x]_2G[X]R[X]_{19}D[X]_7K[X]_{27}G$ (SEQ ID NO: 27), or

   $HXDGAR[X]_3A[X]_{15}D[X]_4CXSK[X]_4PXGS[X]_3G[X]_7A[X]_4K[X]_2GGGXRQXG$ (SEQ ID NO: 28) or

   b)   introduction of a nucleic acid sequence which increases threonine degradation in the transgenic organism, and

   c)   expression of a nucleic acid sequence mentioned under (a) or (b) in the transgenic organism.

3.   (Currently amended) A process for preparing amino acids in transgenic organisms as claimed in claim 1, wherein the process comprises the following steps, solved:

a) introduction of a nucleic acid sequence which codes for a lysine-degrading protein which comprises the following consensus sequence

$G[X]_4GIM[X]_{45}M[X]_2RK[X]_2M[X]_{11}GGXG[X]_3E[X]_2E[X]_3W$ (SEQ ID NO: 29),

or

$LG[X]_9LVYGG[X]_3GIMGXVA[X]_9G[X]_3GXIP[X]_{24}MHXRK[X]_2M[X]_6F[X]_3PGG$

$XGTXEE[X]_2E[X]_2TW[X]_2IG[X]_3KP[X]_4N[X]_3FY[X]_{14}F$ (SEQ ID NO: 30), or

b) introduction of a nucleic acid sequence which increases lysine degradation in the transgenic organisms, and

c) expression of a nucleic acid sequence mentioned under (a) or (b) in the transgenic organism.

4. (Currently amended) A process for preparing amino acids in transgenic organisms as claimed in claim 1, wherein the process comprises the following steps, solved:

a) introduction of a nucleic acid sequence which codes for a threonine-degrading protein which comprises the following consensus sequence

$H[x]_2G[X]R[X]_{19}D[X]_7K[X]_{27}G$ (SEQ ID NO: 27), or

$HXDGAR[X]_3A[X]_{15}D[X]_4CXSK[X]_4PXGS[X]_3G[X]_7A[X]_4K[X]_2GGGXRQXG$ (SEQ ID NO: 28)

and introduction of a nucleic acid sequence which codes for a lysine-degrading protein which comprises the following consensus sequence

$G[X]_4GIM[X]_{45}M[X]_2RK[X]_2M[X]_{11}GGXG[X]_3E[X]_2E[X]_3W$ (SEQ ID NO: 29),

or

$LG[X]_9LVYGG[X]_3GIMGXVA[X]_9G[X]_3GXIP[X]_{24}MHXRK[X]_2M[X]_6F[X]_3PGG$

$XGTXEE[X]_2E[X]_2TW[X]_2IG[X]_3KP[X]_4N[X]_3FY[X]_{14}F$ (SEQ ID NO: 30), or

b)   introduction of a nucleic acid sequence which codes for proteins which increase
threonine degradation and lysine degradation in the transgenic organisms, and

c)   expression of a nucleic acid sequence mentioned under (a) or (b) in the transgenic
organism.

5.   (Previously presented) A process for preparing amino acids in transgenic organisms as
claimed in claim 1, wherein there is introduction in process step (a) as set forth in claim 1
of a nucleic acid sequence which is selected from the group of nucleic acid sequences:

i)   of a nucleic acid sequence having the sequence depicted in SEQ ID NO: 1, SEQ
ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19;
SEQ ID NO: 21; SEQ ID NO: 23 or SEQ ID NO: 25;

ii)   of a nucleic acid sequence obtained owing to the degeneracy of the genetic code
through back-translation of the amino acid sequence depicted in SEQ ID NO: 2,
SEQ ID NO: 12; SEQ ID NO: 14; SEQ ID NO: 16; SEQ ID NO: 18; SEQ ID NO:
20; SEQ ID NO: 22; SEQ ID NO: 24 or SEQ ID NO: 26, and

iii)   of a derivative of the nucleic acid sequence depicted in SEQ ID NO: 1, SEQ ID
NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ
ID NO: 21; SEQ ID NO: 23 or SEQ ID NO: 25; which codes for polypeptides
having the amino acid sequence depicted in SEQ ID NO: 2, SEQ ID NO: 12; SEQ
ID NO: 14; SEQ ID NO: 16; SEQ ID NO: 18; SEQ ID NO: 20; SEQ ID NO: 22;
SEQ ID NO: 24 or SEQ ID NO: 26 and have at least 50% homology at the amino
acid level, with a negligible reduction in the biological activity of the
polypeptides.

6.   (Previously presented) A process for preparing amino acids in transgenic organisms as
claimed in claim 1, wherein there is introduction in process step (a) of a nucleic acid
sequence which is selected from the group of nucleic acid sequences:

i)   of a nucleic acid sequence obtained owing to the degeneracy of the genetic code
through back-translation of the amino acid sequence depicted in SEQ ID NO: 3,

SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9 or SEQ ID NO: 10;

ii) of a derivative of the nucleic acid sequence which is obtained by back-translation of the amino acid sequence depicted in SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9 or SEQ ID NO: 10 and which has at least 70% homology at the amino acid level with the aforementioned amino acid sequences, with a negligible reduction in the biological activity of the polypeptides.

7. (Previously presented) A process for preparing amino acids in transgenic organisms as claimed in claim 1, wherein the transgenic organism is cultivated and harvested after introduction and expression of the nucleic acid.

8. (Previously presented) A process for preparing amino acids in transgenic organisms as claimed in claim 1, wherein the amino acid is isolated from the organism or the culture medium or the organism and the culture medium.

9. (Previously presented) A process for preparing amino acids in transgenic organisms as claimed in claim 1, wherein the essential amino acid methionine is involved.

10. (Previously presented) A process for preparing amino acids in transgenic organisms as claimed in claim 1, wherein the transgenic organism is a microorganism or a plant.

11. (Previously presented) A process for preparing amino acids in transgenic organisms as claimed in claim 10, wherein the transgenic organism is a microorganism selected from the group of genera Corynebacterium, Brevibacterium, Escherichia, Bacillus, Rhodotorula, Hansenula, Schizosaccharomyces, Saccharomyces, Candida, Claviceps or Flavobacterium.

12. (Previously presented) A process for preparing amino acids in transgenic organisms as claimed in claim 10, wherein the transgenic organism is a plant selected from the group of crop plants.

13.   (Original) A process for preparing amino acids in transgenic organisms as claimed in
       claim 12, wherein the transgenic organism is a plant selected from the group of peanut,
       oilseed rape, canola, sunflower, safflower, olive, sesame, hazelnut, almond, avocado, bay,
       pumpkin, lettuce, flax, soybean, pistachio, borage, corn, wheat, rye, oats, millet, triticale,
       rice, barley, cassava, potato, sugar beet, feed beet, aubergine, tomato, pea, alfalfa and
       perennial grasses and feed crops.

14.   (Previously presented) A process for preparing amino acids in transgenic organisms as
       claimed in claim 1, wherein the nucleic acid sequence is derived from a eukaryote.

15.   (Previously presented) A process for preparing amino acids in transgenic organisms as
       claimed in claim 1, wherein the nucleic acid sequence is derived from the genus
       Saccharomyces.

16.   (Previously presented) A process for preparing amino acids in transgenic organisms as
       claimed in claim 1, wherein the nucleic acid sequence is for introduction and for
       expression incorporated into a nucleic acid construct or a vector.

17.   (Previously presented) A process for preparing amino acids in transgenic organisms as
       claimed in claim 1, wherein additionally biosynthesis genes of the amino acid prepared in
       the process are introduced into the organism.

18.   (Currently amended) A nucleic acid construct comprising a nucleic acid sequence
       selected from the group consisting of:

       a)   a nucleic acid which codes for a threonine-degrading protein which comprises the
              following consensus sequence H[x]$_2$G[X]R[X]$_{19}$D[X]$_7$K[X]$_{27}$G (SEQ ID NO: 27),
              or
              HXDGAR[X]$_3$A[X]$_{15}$D[X]$_4$CXSK[X]$_4$PXGS[X]$_3$G[X]$_7$A[X]$_4$K[X]$_2$GGGXRQXG
              (SEQ ID NO: 28)

       b)   a nucleic acid sequence which codes for a lysine-degrading protein which
              comprises the following consensus sequence

G[X]$_4$GIM[X]$_{45}$M[X]$_2$RK[X]$_2$M[X]$_{11}$GGXG[X]$_3$E[X]$_2$E[X]$_3$W (SEQ ID NO: 29),

or

LG[X]$_9$LVYGG[X]$_3$GIMGXVA[X]$_9$G[X]$_3$GXIP[X]$_{24}$MHXRK[X]$_2$M[X]$_6$F[X]$_3$PGG

XGTXEE[X]$_2$E[X]$_2$TW[X]$_2$IG[X]$_3$KP[X]$_4$N[X]$_3$FY[X]$_{14}$F (SEQ ID NO: 30);

c)   a nucleic acid sequence which comprises the nucleic acid sequence under (a) and
      the nucleic acid sequence under (b);

d)   a nucleic acid sequence having the sequence depicted in SEQ ID NO: 1, SEQ ID
      NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ
      ID NO: 21; SEQ ID NO: 23 or SEQ ID NO: 25;

e)   a nucleic acid sequence obtained owing to the degeneracy of the genetic code
      through back-translation of the amino acid sequence depicted in SEQ ID NO: 2,
      SEQ ID NO: 12; SEQ ID NO: 14; SEQ ID NO: 16; SEQ ID NO: 18; SEQ ID NO:
      20; SEQ ID NO: 22; SEQ ID NO: 24 or SEQ ID NO: 26;

f)   a derivative of the nucleic acid sequence depicted in SEQ ID NO: 1, SEQ ID NO:
      11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID
      NO: 21; SEQ ID NO: 23 or SEQ ID NO: 25; which codes for polypeptides having
      the amino acid sequence depicted in SEQ ID NO: 2, SEQ ID NO: 12; SEQ ID
      NO: 14; SEQ ID NO: 16; SEQ ID NO: 18; SEQ ID NO: 20; SEQ ID NO: 22; SEQ
      ID NO: 24 or SEQ ID NO: 26 and have at least 50% homology at the amino acid
      level, with a negligible reduction in the biological activity of the polypeptides;

g)   a nucleic acid sequence obtained owing to the degeneracy of the genetic code
      through back-translation of the amino acid sequence depicted in SEQ ID NO: 3,
      SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8,
      SEQ ID NO: 9 or SEQ ID NO: 10; and

h)   a derivative of the nucleic acid sequence which is obtained by back-translation of
      the amino acid sequence depicted in SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO:

5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9 or SEQ ID NO:
10 and which has at least 70% homology at the amino acid level with the
aforementioned amino acid sequences, with a negligible reduction in the
biological activity of the polypeptides;

wherein the nucleic acid sequence is functionally linked to one or more regulatory
signals.

19.　(Currently amended)　A vector comprising a nucleic acid sequence selected from the
group consisting of:

a)　a nucleic acid which codes for a threonine-degrading protein which comprises the
following consensus sequence $H[x]_2G[X]R[X]_{19}D[X]_7K[X]_{27}G$ (SEQ ID NO: 27),
or

$HXDGAR[X]_3A[X]_{15}D[X]_4CXSK[X]_4PXGS[X]_3G[X]_7A[X]_4K[X]_2GGGXRQXG$
(SEQ ID NO: 28)

b)　a nucleic acid sequence which codes for a lysine-degrading protein which
comprises the following consensus sequence

$G[X]_4GIM[X]_{45}M[X]_2RK[X]_2M[X]_{11}GGXG[X]_3E[X]_2E[X]_3W$ (SEQ ID NO: 29),
or

$LG[X]_9LVYGG[X]_3GIMGXVA[X]_9G[X]_3GXIP[X]_{24}MHXRK[X]_2M[X]_6F[X]_3PGG$

$XGTXEE[X]_2E[X]_2TW[X]_2IG[X]_3KP[X]_4N[X]_3FY[X]_{14}F$ (SEQ ID NO: 30);

c)　a nucleic acid sequence which comprises the nucleic acid sequence under (a) and
the nucleic acid sequence under (b);

d)　a nucleic acid sequence having the sequence depicted in SEQ ID NO: 1, SEQ ID
NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ
ID NO: 21; SEQ ID NO: 23 or SEQ ID NO: 25;

e) a nucleic acid sequence obtained owing to the degeneracy of the genetic code through back-translation of the amino acid sequence depicted in SEQ ID NO: 2, SEQ ID NO: 12; SEQ ID NO: 14; SEQ ID NO: 16; SEQ ID NO: 18; SEQ ID NO: 20; SEQ ID NO: 22; SEQ ID NO: 24 or SEQ ID NO: 26;

f) a derivative of the nucleic acid sequence depicted in SEQ ID NO: 1, SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23 or SEQ ID NO: 25; which codes for polypeptides having the amino acid sequence depicted in SEQ ID NO: 2, SEQ ID NO: 12; SEQ ID NO: 14; SEQ ID NO: 16; SEQ ID NO: 18; SEQ ID NO: 20; SEQ ID NO: 22; SEQ ID NO: 24 or SEQ ID NO: 26 and have at least 50% homology at the amino acid level, with a negligible reduction in the biological activity of the polypeptides;

g) a nucleic acid sequence obtained owing to the degeneracy of the genetic code through back-translation of the amino acid sequence depicted in SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9 or SEQ ID NO: 10; and

h) a derivative of the nucleic acid sequence which is obtained by back-translation of the amino acid sequence depicted in SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9 or SEQ ID NO: 10 and which has at least 70% homology at the amino acid level with the aforementioned amino acid sequences, with a negligible reduction in the biological activity of the polypeptides.

20. (Currently amended) A transgenic prokaryotic or eukaryotic organism comprising at least one nucleic acid sequence selected from the group consisting of:

a) a nucleic acid which codes for a threonine-degrading protein which comprises the following consensus sequence H[x]$_2$G[X]R[X]$_{19}$D[X]$_7$K[X]$_{27}$G (SEQ ID NO: 27), or
HXDGAR[X]$_3$A[X]$_{15}$D[X]$_4$CXSK[X]$_4$PXGS[X]$_3$G[X]$_7$A[X]$_4$K[X]$_2$GGGXRQXG (SEQ ID NO: 28);

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b)   a nucleic acid sequence which codes for a lysine-degrading protein which comprises the following consensus sequence

G[X]$_4$GIM[X]$_{45}$M[X]$_2$RK[X]$_2$M[X]$_{11}$GGXG[X]$_3$E[X]$_2$E[X]$_3$W (SEQ ID NO: 29),

or

LG[X]$_9$LVYGG[X]$_3$GIMGXVA[X]$_9$G[X]$_3$GXIP[X]$_{24}$MHXRK[X]$_2$M[X]$_6$F[X]$_3$PGG

XGTXEE[X]$_2$E[X]$_2$TW[X]$_2$IG[X]$_3$KP[X]$_4$N[X]$_3$FY[X]$_{14}$F (SEQ ID NO: 30);

c)   a nucleic acid sequence which comprises the nucleic acid sequence under (a) and the nucleic acid sequence under (b);

d)   a nucleic acid sequence having the sequence depicted in SEQ ID NO: 1, SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23 or SEQ ID NO: 25;

e)   a nucleic acid sequence obtained owing to the degeneracy of the genetic code through back-translation of the amino acid sequence depicted in SEQ ID NO: 2, SEQ ID NO: 12; SEQ ID NO: 14; SEQ ID NO: 16; SEQ ID NO: 18; SEQ ID NO: 20; SEQ ID NO: 22; SEQ ID NO: 24 or SEQ ID NO: 26;

f)   a derivative of the nucleic acid sequence depicted in SEQ ID NO: 1, SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23 or SEQ ID NO: 25; which codes for polypeptides having the amino acid sequence depicted in SEQ ID NO: 2, SEQ ID NO: 12; SEQ ID NO: 14; SEQ ID NO: 16; SEQ ID NO: 18; SEQ ID NO: 20; SEQ ID NO: 22; SEQ ID NO: 24 or SEQ ID NO: 26 and have at least 50% homology at the amino acid level, with a negligible reduction in the biological activity of the polypeptides;

g)   a nucleic acid sequence obtained owing to the degeneracy of the genetic code through back-translation of the amino acid sequence depicted in SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9 or SEQ ID NO: 10; and

h)   a derivative of the nucleic acid sequence which is obtained by back-translation of

the amino acid sequence depicted in SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO:

5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9 or SEQ ID NO:

10 and which has at least 70% homology at the amino acid level with the

aforementioned amino acid sequences, with a negligible reduction in the

biological activity of the polypeptides.

21.   (Original) A transgenic prokaryotic or eukaryotic organism as claimed in claim 20,

which is a microorganism or a plant.

22.   (Original) A transgenic prokaryotic or eukaryotic organism as claimed in claim 21,

which is a microorganism of the genus Corynebacterium or Brevibacterium.

23.   (Original) A transgenic prokaryotic or eukaryotic organism as claimed in claim 21,

which is a plant selected from the group of genus of peanut, oilseed rape, canola,

sunflower, safflower, olive, sesame, hazelnut, almond, avocado, bay, pumpkin, lettuce,

flax, soybean, pistachio, borage, corn, wheat, rye, oats, millet, triticale, rice, barley,

cassava, potato, sugar beet, feed beet, aubergine, tomato, pea, alfalfa and perennial

grasses and feed crops.

24.   (Previously presented) A process for producing an animal or human food, for producing

cosmetics or pharmaceuticals, comprising growing or culturing the transgenic organism

of claim 20, recovering the amino acid produced, and formulating the amino acid into an

animal or human food, cosmetics or pharmaceuticals.

25.   (Original) An amino acid sequence selected from the group of sequences SEQ ID NO: 3,

SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID

NO: 9 or SEQ ID NO: 10.